## AMENDMENTS TO THE CLAIMS:

The listing of claims will replace all prior versions, and listings, of claims in the application:

Claims 1-11 (Cancelled)

12. (currently amended): A method of high throughput integrated genomics comprising:

a) providing a plurality of enhanced homologous recombination (EHR) compositions, wherein each composition comprises:

i) a recombinase;

ii) a first and a second targeting polynucleotide, wherein said first targeting polynucleotide comprises a portion substantially complementary to a fragment of a target nucleic acid and is substantially complementary to said second targeting polynucleotide; and

iii) a separation moiety;

b) contacting said EHR compositions with a library of target nucleic acid(s) under conditions wherein said targeting polynucleotides hybridize to one or more target nucleic acids of said library; and

c) isolating and cloning said target nucleic acid(s) wherein said isolating and cloning are performed using a robotic system, wherein said robotic system comprises a computer workstation comprising a microprocessor programmed to manipulate a device wherein said device comprises at least one of a gel loading system, a gene sequencer, an automated transformation system, a colony picker, a bead picker, a cell sorter, an incubator, a light microscope, a fluorescence microscope, a spectrofluorimeter, a spectrophotometer, a luminometer and a CCD camera.

13. (Previously presented): The method according to claim 12, wherein said target nucleic acid is a target gene.

14. (Previously presented): The method according to claim 13, wherein said target nucleic acid is a portion of said target gene.

15. (Previously presented): The method according to claim 12, wherein said target nucleic acid is a regulatory sequence.

16. (Previously presented): The method according to claim 12, wherein said target nucleic acid comprises single-polynucleotide polymorphisms.

17. (Previously presented): The method according to claim 12, wherein said library of target nucleic acids comprises all or part of a cDNA library, genomic DNA library, genomic DNA samples, or combinations thereof.

18. (Previously presented): The method of claim 17, wherein said genomic DNA samples are from one or more organisms.

19. (Previously presented): The method according to claim 12 further comprising:

d) making a library of nucleic acid variants of said target nucleic acid;

e) introducing said library of nucleic acid variants into a cellular library; and

f) performing phenotypic screening on said cellular library.

20. (Previously presented): The method according to claim 19 wherein at least one of said making, introducing and performing steps is performed using a robotic system.

21. (Previously presented): The method according to claim 12 further comprising:

d) making a plurality of cells comprising a mutant target nucleic acid;

e) adding a library of candidate agents to said plurality; and

f) determining the effect of said candidate agents on said cells.

22. (Previously presented): The method according to claim 21 wherein at least one of said making, adding, and determining steps is performed using a robotic system.

23. (Previously presented): The method according to claim 21, wherein said mutant target nucleic acid is a gene sequence knock-out or a gene sequence knock-in.

24. (Previously presented): The method according to claim 21, wherein said mutant target nucleic acid comprises an insertion, substitution, deletion or combinations thereof.

Claims 25-27 (Cancelled)

28. (Previously presented): The method according to claim 12 further comprising sequencing said target nucleic acid.

Claims 29-32 (Cancelled)

33. (Presently amended): The method of claim 12, wherein said robotic system comprises a computer workstation comprising a microprocessor programmed to manipulate a device selected from the group consisting of a ~~thermocycler, a multichannel pipettor, a sample handler, a plate handler,~~ a gel loading system, a gene sequencer, an automated transformation system, a colony picker, a bead picker, a cell sorter, an incubator, a light microscope, a fluorescence microscope, a spectrofluorimeter, a spectrophotometer, a luminometer, a CCD camera and combinations thereof.

34-38. (Cancelled)

49. (Previously presented): The method of claim 17, wherein said genomic library comprises nucleic acid from a combination of multiple organisms.

Claims 50-51 (Cancelled)

Claim 52 (new): The method of Claim 12 wherein said device comprises a gel loading system.

Claim 53 (new): The method of Claim 12 wherein said device comprises a gene sequencer.

Claim 54 (new): The method of Claim 12 wherein said device comprises an automated transformation system.

Claim 55 (new): The method of Claim 12 wherein said device comprises a colony picker.

Claim 56 (new): The method of Claim 12 wherein said device comprises a bead picker.

Claim 57 (new): The method of Claim 12 wherein said device comprises a cell sorter.

Claim 58 (new): The method of Claim 12 wherein said device comprises an incubator.

Claim 59 (new): The method of Claim 12 wherein said device comprises a fluorescence microscope.

Claim 60 (new): The method of Claim 12 wherein said device comprises a spectrofluorimeter.

Claim 61 (new): The method of Claim 12 wherein said device comprises a spectrophotometer.

Claim 62 (new): The method of Claim 12 wherein said device comprises a luminometer.

Claim 63 (new): The method of Claim 12 wherein said device comprises a CCD camera.

Claim 64 (new): The method of Claim 12 wherein said device comprises a automated transformation system and a spectrofluorimeter.